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#Simulates human for 2 weeks using mouse study protocol (6 hr/day 5
days/week)
#Uses metabolism constants from Yang et al. 2012 Table 3

#Set the working directory to where you downloaded the scripts
setwd(dirname(parent.frame(2)$ofile))

#Load libraries needed to run scenario
library(deSolve)

#Model path and name
mName <- "chloroprene.model"

#Load model inits file for the ode solver
source(paste0(mName, "_inits.R"))

#Load the model dll
dyn.load(paste0(mName, .Platform$dynlib.ext))

#Scenario specific values
tstart <- 0.0
tstop <- 336
times <- seq(tstart, tstop , by=0.01)

#Physiological parameters path
#Load the parameters
source('./params/Human.R')    #Revised parameters from June 27 2018 update
source('./states.R')

*****#
*****#
#Simulation specific metabolism parameters
parms ["VMAXC"] <- 17.53# Liver
parms ["KM"] <- 0.034

parms ["VMAXCLU"] <- 0.0034    # Lung
parms ["KMLU"] <- 0.034
parms ["KFLUC"] <- 0.0          #Upper 95th percentile posterior
distribution
parms ["KFLUC"] <- 2.60e-12    #geometric mean posterior distribution

parms ["VMAXCKid"] <- 0.0    # Kidney
parms ["KMKD"] <- 1.0
parms ["KFKIC"] <- 0.0
*****#
*****#

#Timing variables for forcing functions
dstart <- tstart
dlength <- 24      #hours per day to expose
ddaysperwk <- 7   #days of week to expose
dexpend <- 100    #days of exposure
parms ["TSTOP"] <- tstop

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#Source forcing functions
#This loads the function forcing() in the namespace
source("forfunc.R")

#Scenario Specific Exposure
parms ["CONC"]<- 12.8

ppm <- c(0.00028, 0.001, 0.005, 0.01, 0.05, 0.1, 0.5, 1, 5, 10, 50, 100)
cinh1 <- data.frame(ppm)
cinh <- lapply(cinh1, as.numeric)
outlist <- list()
ppm2 <- list()

for(i in 1:nrow(cinh1)){
  parms ["CONC"] <- cinh1[i,]

  {
    out <-ode(Y, times, func = "derivs", parms = parms,
method="vode", atol=1.0e-10, rtol=1.0e-8,
              dllname = mName, initforc="initforc", forcings=forcings,
initfunc = "initmod", nout = length(Outputs),
              fcontrol=list(method="linear")), outnames = Outputs)

    }
    outlist[[i]] <- out[33601,]
  }
frout1 <- data.frame(outlist)
dout <- data.frame(t(frout1), row.names=paste(1:12))
rout <- cbind(dout[,c(21,22,23,24)]) 

#displays the output
"Human Continuous - MY Redo"
rout

#unload the model dll
dyn.unload(paste0(mName,.Platform$dynlib.ext))

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